

\$%^STN;HighlightOn= \*\*\*;HighlightOff=\*\*\* ;

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NEWS	2	"Ask CAS" for self-help around the clock
NEWS	3	May 12 EXTEND option available in structure searching
NEWS	4	May 12 Polymer links for the POLYLINK command completed in REGISTRY
NEWS	5	May 27 New UPM (Update Code Maximum) field for more efficient patent SDIs in CPlus
NEWS	6	May 27 CPlus super roles and document types searchable in REGISTRY
NEWS	7	Jun 28 Additional enzyme-catalyzed reactions added to CASREACT
NEWS	8	Jun 28 ANTE, AQUALINE, BIOENG, CIVILENG, ENVIROENG, MECHENG, and WATER from CSA now available on STN(R)
NEWS	9	Jul 12 BEILSTEIN enhanced with new display and select options, resulting in a closer connection to BABS
NEWS	10	Jul 30 BEILSTEIN on STN workshop to be held August 24 in conjunction with the 228th ACS National Meeting
NEWS	11	AUG 02 IFIPAT/IFIUDB/IFICDB reloaded with new search and display fields
NEWS	12	AUG 02 CPlus and CA patent records enhanced with European and Japan Patent Office Classifications
NEWS	13	AUG 02 STN User Update to be held August 22 in conjunction with the 228th ACS National Meeting
NEWS	14	AUG 02 The Analysis Edition of STN Express with Discover! (Version 7.01 for Windows) now available
NEWS	15	AUG 04 Pricing for the Save Answers for SciFinder Wizard within STN Express with Discover! will change September 1, 2004
NEWS EXPRESS	JULY 30	CURRENT WINDOWS VERSION IS V7.01, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004
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=> file ca

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

FILE 'CA' ENTERED AT 11:32:13 ON 19 AUG 2004

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FILE COVERS 1907 - 13 Aug 2004 VOL 141 ISS 8  
FILE LAST UPDATED: 13 Aug 2004 (20040813/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> e norris b j/au

E1	10	NORRIS B C/AU
E2	1	NORRIS B D/AU
E3	10 -->	NORRIS B J/AU
E4	3	NORRIS B L/AU
E5	4	NORRIS B S/AU
E6	4	NORRIS BARBARA/AU
E7	7	NORRIS BARBARA J/AU
E8	1	NORRIS BARBARA JANE/AU
E9	1	NORRIS BARBARA L/AU
E10	3	NORRIS BARRY L/AU
E11	2	NORRIS BELINDA/AU
E12	3	NORRIS BELINDA J/AU

=> e

E13	2	NORRIS BERRY E/AU
E14	23	NORRIS BERYL/AU
E15	2	NORRIS BERYL C/AU
E16	3	NORRIS BEVERLY/AU
E17	6	NORRIS BEVERLY J/AU
E18	1	NORRIS BOBBY E/AU
E19	1	NORRIS BOBBY E JR/AU

E20 1 NORRIS BRADLEY J/AU  
 E21 3 NORRIS BRENT A/AU  
 E22 9 NORRIS BRIAN/AU  
 E23 4 NORRIS BRIAN D/AU  
 E24 2 NORRIS BRIAN J/AU

=> s e3 11-12  
 MISSING OPERATOR

=> s e3 or e11-12  
 10 "NORRIS B J"/AU  
 2 "NORRIS BELINDA"/AU  
 3 "NORRIS BELINDA J"/AU  
 L1 15 "NORRIS B J"/AU OR ("NORRIS BELINDA"/AU OR "NORRIS BELINDA J"/AU  
 )

=> s l1 and py=1994  
 700004 PY=1994  
 L2 1 L1 AND PY=1994

=> d

L2 ANSWER 1 OF 1 CA COPYRIGHT 2004 ACS on STN  
 AN 121:51029 CA  
 TI Nucleotide sequence of a cDNA clone encoding the precursor of the  
 peridinin-chlorophyll a-binding protein from the dinoflagellate  
 Symbiodinium sp.  
 AU \*\*\*Norris, Belinda J.\*\*\* ; Miller, David J.  
 CS Dep. Mol. Sci., James Cook Univ. North Queensland, Queensland, 4811,  
 Australia  
 SO Plant Molecular Biology ( \*\*\*1994\*\*\* ), 24(4), 673-7  
 CODEN: PMBIDB; ISSN: 0167-4412  
 DT Journal  
 LA English

=> d ind

L2 ANSWER 1 OF 1 CA COPYRIGHT 2004 ACS on STN  
 CC 3-3 (Biochemical Genetics)  
 Section cross-reference(s): 6, 10  
 ST peridinin chlorophyll binding protein cDNA Symbiodinium; sequence peridin  
 chlorophyll binding protein Symbiodinium  
 IT Gene, microbial  
 RL: BIOL (Biological study)  
 (for peridinin-chlorophyll a-binding protein, of Symbiodinium,  
 nucleotide and encoded peptide sequences of)  
 IT Protein sequences  
 (of peridinin-chlorophyll a-binding protein and precursor, of  
 Symbiodinium)  
 IT Symbiodinium  
 (peridinin-chlorophyll a-binding protein of, nucleotide sequence of of  
 cDNA for)  
 IT Deoxyribonucleic acid sequences  
 (complementary, for peridinin-chlorophyll a-binding protein, of  
 Symbiodinium)  
 IT 156287-89-7, Peridinin-chlorophyll a-binding protein (Symbiodinium clone

PCP1a)  
 RL: PRP (Properties)  
 (amino acid sequence of)  
 IT 33281-81-1, Peridinin  
 RL: PRP (Properties)  
 (binding protein for chlorophyll a and, of Symbiodinium, nucleotide  
 sequence of cDNA for)  
 IT 479-61-8, Chlorophyll a  
 RL: PRP (Properties)  
 (binding protein for peridinin and, of Symbiodinium, nucleotide  
 sequence of cDNA for)  
 IT 152021-28-8  
 RL: PRP (Properties); BIOL (Biological study)  
 (nucleotide sequence of)

=> FIL REGISTRY

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	10.33	10.54

FILE 'REGISTRY' ENTERED AT 11:35:28 ON 19 AUG 2004  
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STRUCTURE FILE UPDATES: 18 AUG 2004 HIGHEST RN 728239-10-9  
 DICTIONARY FILE UPDATES: 18 AUG 2004 HIGHEST RN 728239-10-9

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when  
 conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more  
 information enter HELP PROP at an arrow prompt in the file or refer  
 to the file summary sheet on the web at:  
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> S 156287-89-7/RN

L3 1 156287-89-7/RN

=> SET NOTICE 1 DISPLAY

NOTICE SET TO 1 U.S. DOLLAR FOR DISPLAY COMMAND  
 SET COMMAND COMPLETED

=> D L3 SQIDE 1-

YOU HAVE REQUESTED DATA FROM 1 ANSWERS - CONTINUE? Y/(N):y

THE ESTIMATED COST FOR THIS REQUEST IS 5.92 U.S. DOLLARS  
DO YOU WANT TO CONTINUE WITH THIS REQUEST? (Y)/N:y

L3 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN  
RN \*\*\*156287-89-7\*\*\* REGISTRY  
CN Protein (Symbiodinium clone PCP1a chlorophyll a-peridinin-containing)  
(9CI) (CA INDEX NAME)  
FS PROTEIN SEQUENCE  
SQL 365

SEQ 1 MVRGARKAIA VGVAVAVACG LQKHLNFVPG PRHAAPVAAA AASMMAPAA  
51 FADEIGDAAK KLGDASYFA KEVDWNNGIF LQAPGKFQPL EALKAIKMI  
101 EMGAAADPKL LKDAEAHKK AIGSISGPNV VTSRADWDAV NAAIGRVVAS  
151 VPKAKVMNAVY DSVTAITDPG VPAYMKSLVN GPDAEKAYQG FLEFKDVVEK  
201 NQVATASAPA VVPSGDKIGE AAKALSDASY PFIKDIDWLS DIYLPKPLPGK  
251 TAPETLKAID KMIVMGAKMD GNLLKAAAEA HHKAIGSIDA TGVTSADYE  
301 AVNAAIGRLV ASVPKTTVMD VYNMAGVVD SSVNNLFSK VNPLDAVAAA  
351 KGFYTFKDVV EASQR

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA CAPLUS document type: Conference; Journal

RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence); PRP  
(Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> SET NOTICE LOGIN DISPLAY

NOTICE SET TO OFF FOR DISPLAY COMMAND

SET COMMAND COMPLETED

=>

=> e Peridinin-chlorophyll a-binding protein/cn

E1 1 PERIDININ ACETATE/CN  
E2 1 PERIDININ P-BROMOBENZOATE/CN  
E3 0 --> PERIDININ-CHLOROPHYLL A-BINDING PROTEIN/CN  
E4 1 PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE P  
RGH150 GENE HETE2 PRECURSOR)/CN  
E5 1 PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE P  
RGH151 GENE HETE7 PRECURSOR)/CN  
E6 1 PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE P  
RGH152 C-TERMINAL FRAGMENT)/CN  
E7 1 PERIDININOL/CN  
E8 1 PERIDINOSTEROL/CN  
E9 1 PERIDINOSTERONE/CN  
E10 1 PERIDOL/CN  
E11 1 PERIDON/CN  
E12 1 PERIDOT/CN

=> set expand cont

SET COMMAND COMPLETED

=> e peridin/cn

E13	1	PERIDEX (ANTISEPTIC)/CN
E14	1	PERIDEX LA/CN
E15	1 -->	PERIDININ/CN
E16	1	PERIDININ ACETATE/CN
E17	1	PERIDININ P-BROMOBENZOATE/CN
E18	1	PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE P RGH150 GENE HETE2 PRECURSOR)/CN
E19	1	PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE P RGH151 GENE HETE7 PRECURSOR)/CN
E20	1	PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE P RGH152 C-TERMINAL FRAGMENT)/CN
E21	1	PERIDININOL/CN
E22	1	PERIDINOSTEROL/CN
E23	1	PERIDINOSTERONE/CN
E24	1	PERIDOL/CN

=> s e18-20

	1	"PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE PRGH150 GENE HETE2 PRECURSOR)"/CN
	1	"PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE PRGH151 GENE HETE7 PRECURSOR)"/CN
	1	"PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE PRGH152 C-TERMINAL FRAGMENT)"/CN
L4	3	("PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE PRGH150 GENE HETE2 PRECURSOR)"/CN OR "PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE PRGH151 GENE HETE7 PRECURSO R)"/CN OR "PERIDININ-CHLOROPHYLL A-PROTEIN (HETEROCAPSA PYGMAEA CLONE PRGH152 C-TERMINAL FRAGMENT)"/CN)

=> file ca

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
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FILE 'CA' ENTERED AT 11:39:08 ON 19 AUG 2004

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FILE COVERS 1907 - 13 Aug 2004 VOL 141 ISS 8

FILE LAST UPDATED: 13 Aug 2004 (20040813/ED)

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=> s l3 or l4

2 L3

1 L4

L5 3 L3 OR L4

=> d bib abs 1-3

L5 ANSWER 1 OF 3 CA COPYRIGHT 2004 ACS on STN

AN 136:364547 CA

TI The 15-kDa forms of the apo-peridinin-chlorophyll a protein (PCP) in dinoflagellates show high identity with the apo-32 kDa PCP forms, and have similar N-terminal leaders and gene arrangements

AU Hiller, R. G.; Crossley, L. G.; Wrench, P. M.; Santucci, N.; Hofmann, E.

CS Department of Biological Sciences, Macquarie University, Sydney, 2109, Australia

SO Molecular Genetics and Genomics (2001), 266(2), 254-259

CODEN: MGGOAA; ISSN: 1617-4615

PB Springer-Verlag

DT Journal

LA English

AB Full-length genomic sequences encoding apo peridinin-chlorophyll a proteins (PCPs) from *Heterocapsa pygmaea* have been obtained by PCR. Two of the derived mature proteins of 150 residues have mol. masses of 15,795 and 15,780, resp. Contrary to an earlier report, these show a high degree of identity (.apprx.70%) over the whole of both domains to the mature 32-kDa PCP forms. The two genes lack introns, are arranged in tandem and sepd. by 526 bp. A putative N-terminal extension with three domains characteristic of a signal sequence, a chloroplast-targeting sequence and a thylakoid lumen-directing sequence, is present. Modeling of the *Heterocapsa* PCP amino acid sequence on to the high-resoln. structure available for *Amphidinium* PCP shows that the main differences between two forms are in trimer contact regions.

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 3 CA COPYRIGHT 2004 ACS on STN

AN 130:194046 CA

TI A comparison of the protein profiles of cultured and endosymbiotic *Symbiodinium bermudense* from the anemone *Aiptasia pallida*

AU Stochaj, Wayne R.; Grossman, Arthur R.

CS Department of Plant Biology, Carnegie Institution of Washington, Stanford, CA, 94305, USA

SO Proceedings of the International Coral Reef Symposium, 8th, Panama, June 24-29, 1996 (1997), Volume 2, 1325-1330. Editor(s): Lessios, Harilaos A.; Macintyre, Ian G. Publisher: Smithsonian Tropical Research Institute, Balboa, Panama.

CODEN: 67CLAW

DT Conference

LA English

AB SDS-PAGE and immunol. analyses were used to visualize differences in the protein profile of *S. bermudense* when grown in the cultured and endosymbiotic states (freshly isolated zooxanthellae). Major differences were found between proteins expressed in these 2 states. Using monospecific antibodies, differences in specific proteins synthesized by the symbiotic and cultured *S. bermudense* were demonstrated. These include

changes in the extrinsic peridinin-chlorophyll a binding protein, the form II RuBP carboxylase, and the putative integral membrane peridinin-chlorophyll a c binding protein. These results demonstrate that there are dramatic changes in the population of proteins synthesized when *S. bermudense* adapt to the symbiotic habitat. Such change may reflect a developmental switch that tailors the physiol. of the algae to an endosymbiotic mode of growth.

RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 3 CA COPYRIGHT 2004 ACS on STN  
AN 121:51029 CA  
TI Nucleotide sequence of a cDNA clone encoding the precursor of the peridinin-chlorophyll a-binding protein from the dinoflagellate *Symbiodinium* sp.  
AU Norris, Belinda J.; Miller, David J.  
CS Dep. Mol. Sci., James Cook Univ. North Queensland, Queensland, 4811, Australia  
SO Plant Molecular Biology (1994), 24(4), 673-7  
CODEN: PMBIDB; ISSN: 0167-4412  
DT Journal  
LA English  
AB MRNA from the dinoflagellate *Symbiodinium* sp. isolated from the staghorn coral *Acropora formosa* was used for the construction of cDNA libraries. A cDNA clone was identified which encoded the precursor of peridinin-chlorophyll a-binding protein (PCP), including a 52 amino acid transit peptide and the 313 amino acid mature protein. The deduced amino acid sequence clearly contains an internal duplication, implying that amongst dinoflagellates the Mr 35000 form of PCP has arisen by duplication and fusion of genes encoding the Mr 15000 form. This is the first reported sequence of a dinoflagellate light-harvesting protein. The anatomy of the mature protein and the transit peptide are discussed.

=> file reg

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	8.94	41.21
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.98	-1.98

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STRUCTURE FILE UPDATES: 18 AUG 2004 HIGHEST RN 728239-10-9  
DICTIONARY FILE UPDATES: 18 AUG 2004 HIGHEST RN 728239-10-9

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> sel name l3

E25 THROUGH E25 ASSIGNED

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
1.56	42.77

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
0.00	-1.98

CA SUBSCRIBER PRICE

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, AQUALINE, ANABSTR, ANTE, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DGENE, ...' ENTERED AT 11:42:56 ON 19 AUG

2004

74 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s Peridinin-chlorophyll a-binding protein

3 FILE AGRICOLA

4 FILE AQUASCI

2 FILE BIOENG

5 FILE BIOSIS

14 FILES SEARCHED...

2 FILE BIOTECHNO

8 FILE CAPLUS

22 FILES SEARCHED...

1 FILE DISSABS

28 FILES SEARCHED...

2 FILE EMBASE

4 FILE ESBIODBASE

36 FILES SEARCHED...

54 FILE GENBANK

5 FILE LIFESCI

4 FILE MEDLINE

52 FILES SEARCHED...

1 FILE OCEAN

1 FILE PASCAL

7 FILE SCISEARCH

24 FILE USPATFULL

67 FILES SEARCHED...

16 FILES HAVE ONE OR MORE ANSWERS, 74 FILES SEARCHED IN STNINDEX

L6 QUE PERIDININ-CHLOROPHYLL A-BINDING PROTEIN

=> d rank

F1	54	GENBANK
F2	24	USPATFULL
F3	8	CAPLUS
F4	7	SCISEARCH
F5	5	BIOSIS
F6	5	LIFESCI
F7	4	AQUASCI
F8	4	ESBIOBASE
F9	4	MEDLINE
F10	3	AGRICOLA
F11	2	BIOENG
F12	2	BIOTECHNO
F13	2	EMBASE
F14	1	DISSABS
F15	1	OCEAN
F16	1	PASCAL

=> file f3-16

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	6.84	49.61
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-1.98

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FILE 'BIOENG' ENTERED AT 11:50:16 ON 19 AUG 2004

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=> s l6

6 FILES SEARCHED...

11 FILES SEARCHED...

L7 49 L6

=> dup rem l7

PROCESSING COMPLETED FOR L7

L8 11 DUP REM L7 (38 DUPLICATES REMOVED)

ANSWERS '1-8' FROM FILE CAPLUS

ANSWERS '9-10' FROM FILE SCISEARCH

ANSWER '11' FROM FILE DISSABS

=> d bib abs 1-11

L8 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

AN 2004:72944 CAPLUS

DN 140:247956

TI PCP gene family in Symbiodinium from Hippopus hippopus: Low levels of  
concerted evolution, isoform diversity, and spectral tuning of  
chromophores

AU Reichman, Jay R.; Wilcox, Thomas P.; Vize, Peter D.

CS School of Biological Sciences, University of Texas at Austin, USA

SO Molecular Biology and Evolution (2003), 20(12), 2143-2154

CODEN: MBEVEO; ISSN: 0737-4038

PB Oxford University Press

DT Journal

LA English

AB Photosynthetic dinoflagellates have evolved unique water-sol. light  
harvesting complexes known as \*\*\*peridinin\*\*\* - \*\*\*chlorophyll\*\*\*  
\*\*\*a\*\*\* - \*\*\*binding\*\*\* \*\*\*proteins\*\*\* (PCPs). Most species of  
dinoflagellates express either 14 to 17 kDa or 32 to 35 kDa mature PCP  
apoproteins and do so in stable combinations of isoforms that differ in  
isoelec. point (pI). The source (posttranslational modification, protein  
degrdn., or genetic) and functional significance of PCP isoform variation  
have remained unclear. PCPs are encoded by multigene families. However,  
previous reports conflict over the diversity of PCP genes within gene

arrays. The authors present the first genomic characterization of the PCP gene family from a symbiotic dinoflagellate. Symbiodinium from the Pacific bivalve *Hippopus hippopus* (203) contains genes for 33 kDa PCP apoproteins that are organized in tandem arrays like those of free-living dinoflagellates *Amphidinium carterae*, *Lingulodinium* (*Gonyaulax*) *polyedra*, and *Heterocapsa pygmaea*. The Symbiodinium 203 PCP cassette consists of 1,098-bp coding regions sepd. by approx. 900-bp spacers. The spacers contain a conserved upstream sequence similar to the promoter in *L. polyedra*. Surprisingly, sequences of cloned coding regions are not identical, and can differ at up to 2.2% of the nucleotide sites. Sequence variation is found at both silent and nonsilent sites, and anal. of cDNA clones indicate that the variation is present in the mRNA pool. The authors propose that this variation represents nucleotide diversity among PCP gene copies that are evolving under low-level concerted evolution. Interestingly, the predicted proteins have pIs that are within the range of those published for other species of Symbiodinium. Thus, posttranslational modifications are not necessary to explain the multiple PCP isoforms. The authors have also identified several polymorphic sites that may influence spectral absorption tuning of chromophores.

RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2  
AN 1997:639286 CAPLUS  
DN 127:327183  
TI Structure and organization of the \*\*\*peridinin\*\*\* - \*\*\*chlorophyll\*\*\*  
\*\*\*a\*\*\* - \*\*\*binding\*\*\* \*\*\*protein\*\*\* gene in *Gonyaulax polyedra*  
AU Le, Q. H.; Markovic, P.; Hastings, J. W.; Jovine, R. V. M.; Morse, D.  
CS Inst. Recherche Biol. Vegetale, Univ. Montreal, Montreal, QC, H1X 2B2,  
Can.  
SO Molecular & General Genetics (1997), 255(6), 595-604  
CODEN: MGGEAE; ISSN: 0026-8925  
PB Springer  
DT Journal  
LA English  
AB The authors have identified a major 32-kDa protein in the dinoflagellate *Gonyaulax polyedra* as a \*\*\*peridinin\*\*\* - \*\*\*chlorophyll\*\*\*  
\*\*\*a\*\*\* - \*\*\*binding\*\*\* \*\*\*protein\*\*\* (PCP), based on  
microsequence data and immunol. cross-reaction with antibodies raised  
against PCP from another dinoflagellate species. A cDNA for this protein,  
identified by a PCR-based cloning strategy, encoded all 68 of the amino  
acids microsequenced, thus confirming the identity of the clone. The PCP  
gene is highly expressed at both the mRNA and protein levels, and only PCP  
transcripts corresponding in size to the cDNA sequence were detected.  
Slot blot analyses show that there are roughly 5000 copies of the PCP gene  
in *Gonyaulax*, making this gene one of the most highly repeated  
protein-coding genes ever reported, yet the sequence of the different gene  
copies in the genome appears extraordinary well conserved as judged by  
Southern blot analyses. The gene, as indicated by Southern blot and PCR  
data, is suggested to be present in 5000 intronless copies arranged head  
to tail in the genome, sepd. by conserved 1-kb spacers. Based on the  
conserved sequence of the spacer region, its presence next to each of the  
PCP coding sequences, and the uniform size of the PCP transcript, the  
authors propose that this region represents a dinoflagellate  
transcriptional promoter. This putative promoter region contains none of  
the sequence elements for DNA-binding proteins involved in transcriptional  
initiation reported in other organisms.

L8 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3  
 AN 1997:213077 CAPLUS  
 DN 126:209367  
 TI Differences in the protein profiles of cultured and endosymbiotic  
 Symbiodinium sp. (Pyrrophyta) from the anemone Aiptasia pallida (Anthozoa)  
 AU Stocha, Wayne R.; Grossman, Arthur R.  
 CS Department of Plant Biology, Carnegie Institution of Washington, Stanford,  
 CA, 94305, USA  
 SO Journal of Phycology (1997), 33(1), 44-53  
 CODEN: JPYLAJ; ISSN: 0022-3646  
 PB Phycological Society of America  
 DT Journal  
 LA English  
 AB One- and two-dimensional sodium dodecylsulfate-polyacrylamide gel  
 electrophoresis and immunol. analyses were used to visualize differences  
 in polypeptides synthesized by Symbiodinium sp. from the anemone Aiptasia  
 pallida when grown in the cultured and endosymbiotic states (freshly  
 isolated zooxanthellae). Surprisingly, a comparison of proteins in  
 cultured and endosymbiotic Symbiodinium sp. revealed only four major  
 polypeptides with similar isoelec. and mol. mass characteristics. Using  
 monospecific antibodies, we demonstrated differences in specific proteins  
 synthesized by the dinoflagellate in the two different growth states. The  
 dimeric, 14 kDa form of the peripheral membrane \*\*\*peridinin\*\*\* -  
 \*\*\*chlorophyll\*\*\* \*\*\*a\*\*\* \*\*\*binding\*\*\* \*\*\*protein\*\*\*  
 predominates under endosymbiotic conditions, whereas the monomeric, 35 kDa  
 form predominates under the culture conditions used in this study.  
 Antibodies to form II ribulose-1,5-bisphosphate carboxylase revealed 62  
 and 60 kDa forms of this protein in the alga grown as an endosymbiont and  
 in culture, resp. Differences in the integral membrane  
 peridinin-chlorophyll a-c-binding proteins were also obsd. These results  
 demonstrate that there are major changes in the populations of proteins  
 synthesized by Symbiodinium sp. in response to the conditions in hospite.  
 Such changes may reflect a developmental switch that tailors the physiol.  
 of the alga to the conditions encountered in the endosymbiotic state.

L8 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4  
 AN 1995:521503 CAPLUS  
 DN 123:162534  
 TI Nucleotide sequence of two cDNAs encoding fucoxanthin chlorophyll a/c  
 proteins in the diatom Odontella sinensis  
 AU Kroth-Pancic, Peter G.  
 CS Institut fuer Biochemie der Pflanzen, Heinrich-Heine-Universitaet  
 Duesseldorf, Duesseldorf, 40225, Germany  
 SO Plant Molecular Biology (1995), 27(4), 825-8  
 CODEN: PMBIDB; ISSN: 0167-4412  
 PB Kluwer  
 DT Journal  
 LA English  
 AB Two cDNA clones encoding fucoxanthin chlorophyll a/c-binding proteins  
 (FCP) in the diatom Odontella sinensis were cloned and sequenced. The  
 derived amino acid sequences of both clones are identical, comparison of  
 the corresponding nucleic acids reveals differences only in the third  
 codon position, suggesting a recent gene duplication. The derived  
 proteins are similar to the chlorophyll a/b-binding proteins of higher  
 plants. The presequences for plastid import resemble signal sequences for  
 cotranslational import rather than transit peptides of higher plants.

They are very similar to the presequences of FCP proteins in the diatom *Phaeodactylum*, but different from the presequences of the .gamma.-subunit of C<sub>Fo</sub>C<sub>F1</sub> of *Odontella* and the \*\*\*peridinin\*\*\* \*\*\*chlorophyll\*\*\*  
 \*\*\*a\*\*\* \*\*\*binding\*\*\* \*\*\*proteins\*\*\* (PCP) of the  
 dinoflagellate  
*Symbiodinium*.

L8 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5  
 AN 1994:451029 CAPLUS  
 DN 121:51029  
 TI Nucleotide sequence of a cDNA clone encoding the precursor of the  
 \*\*\*peridinin\*\*\* - \*\*\*chlorophyll\*\*\* \*\*\*a\*\*\* - \*\*\*binding\*\*\*  
 \*\*\*protein\*\*\* from the dinoflagellate *Symbiodinium* sp.  
 AU Norris, Belinda J.; Miller, David J.  
 CS Dep. Mol. Sci., James Cook Univ. North Queensland, Queensland, 4811,  
 Australia  
 SO Plant Molecular Biology (1994), 24(4), 673-7  
 CODEN: PMBIDB; ISSN: 0167-4412  
 DT Journal  
 LA English  
 AB MRNA from the dinoflagellate *Symbiodinium* sp. isolated from the staghorn coral *Acropora formosa* was used for the construction of cDNA libraries. A cDNA clone was identified which encoded the precursor of \*\*\*peridinin\*\*\*  
 - \*\*\*chlorophyll\*\*\* \*\*\*a\*\*\* - \*\*\*binding\*\*\* \*\*\*protein\*\*\*  
 (PCP), including a 52 amino acid transit peptide and the 313 amino acid mature protein. The deduced amino acid sequence clearly contains an internal duplication, implying that amongst dinoflagellates the Mr 35000 form of PCP has arisen by duplication and fusion of genes encoding the Mr 15000 form. This is the first reported sequence of a dinoflagellate light-harvesting protein. The anatomy of the mature protein and the transit peptide are discussed.

L8 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 6  
 AN 1991:117205 CAPLUS  
 DN 114:117205  
 TI Tetrameric native structure of the \*\*\*peridinin\*\*\* - \*\*\*chlorophyll\*\*\*  
 \*\*\*a\*\*\* - \*\*\*binding\*\*\* \*\*\*protein\*\*\* from *Symbiodinium* sp  
 AU Gerberding, Holger; Norris, Belinda; Miller, David J.; Mayer, Frank  
 CS Inst. Mikrobiol., Georg-August-Univ., Goettingen, D-3400, Germany  
 SO Journal of Plant Physiology (1991), 137(3), 285-90  
 CODEN: JPPHEY; ISSN: 0176-1617  
 DT Journal  
 LA English  
 AB Electron microscopy of a single isoform of the peridin-chlorophyll  
 a-binding protein from *Symbiodinium* sp. indicates that the native structure is a tetrahedron-like assembly of four subunits. The subunits are elongated and have a somewhat bent appearance. Based on the EM observations, a working model is proposed that has two orthogonally-arranged dimers in contact via their concave surfaces.

L8 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1999:5113 CAPLUS  
 DN 130:194046  
 TI A comparison of the protein profiles of cultured and endosymbiotic  
*Symbiodinium bermudense* from the anemone *Aiptasia pallida*  
 AU Stochaj, Wayne R.; Grossman, Arthur R.  
 CS Department of Plant Biology, Carnegie Institution of Washington, Stanford,

CA, 94305, USA

SO Proceedings of the International Coral Reef Symposium, 8th, Panama, June 24-29, 1996 (1997), Volume 2, 1325-1330. Editor(s): Lessios, Harilaos A.; Macintyre, Ian G. Publisher: Smithsonian Tropical Research Institute, Balboa, Panama.  
CODEN: 67CLAW

DT Conference

LA English

AB SDS-PAGE and immunol. analyses were used to visualize differences in the protein profile of *S. bermudense* when grown in the cultured and endosymbiotic states (freshly isolated zooxanthellae). Major differences were found between proteins expressed in these 2 states. Using monospecific antibodies, differences in specific proteins synthesized by the symbiotic and cultured *S. bermudense* were demonstrated. These include changes in the extrinsic \*\*\*peridinin\*\*\* - \*\*\*chlorophyll\*\*\*  
\*\*\*a\*\*\* \*\*\*binding\*\*\* \*\*\*protein\*\*\*, the form II RuBP carboxylase, and the putative integral membrane peridinin-chlorophyll a c binding protein. These results demonstrate that there are dramatic changes in the population of proteins synthesized when *S. bermudense* adapt to the symbiotic habitat. Such change may reflect a developmental switch that tailors the physiol. of the algae to an endosymbiotic mode of growth.

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L8 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1994:573247 CAPLUS

DN 121:173247

TI Characterization of two full-length cDNA sequences encoding for apoproteins of peridinin-chlorophyll a-protein (PCP) complexes

AU Triplett, Edward L.; Jovine, Raffael V. M.; Govind, Nadathur S.; Roman, Steven J.; Chang, Suknan S.; Prezelin, Barbara B.

CS Mar. Sci. Inst., Univ. California, Santa Barbara, CA, 93106, USA

SO Molecular Marine Biology and Biotechnology (1993), 2(4), 246-54  
CODEN: MMBBEQ; ISSN: 1053-6426

DT Journal

LA English

AB Characterizations are presented for RNA, 2 cDNA libraries, and 2 full-length cDNA sequences encoding photosynthetic light-harvesting peridinin-chlorophyll a-protein (PCP) in the dinoflagellate *Heterocapsa pygmaea*. Subsequent analyses of the PCP system also indicate that (1) it is represented by multiple nuclear encoded genes, (2) a subset of mRNAs encoding for PCP apoproteins are regulated by growth irradiance, (3) PCP preproteins are larger than the mature apoproteins, and (4) PCP cDNA clones sequenced thus far contain a conserved region but are not identical. Results are discussed in the context of photoadaptation in dinoflagellates.

L8 ANSWER 9 OF 11 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

AN 92:553900 SCISEARCH

GA The Genuine Article (R) Number: JN475

TI QUANTIFICATION OF CHROMOPHORE PIGMENTS, APOPROTEIN ABUNDANCE AND ISOLECTRIC VARIANTS OF PERIDININ-CHLOROPHYLL A-PROTEIN COMPLEXES (PCPS) IN THE DINOFLAGELLATE HETEROCAPSA-PYGMAEA GROWN UNDER VARIABLE LIGHT CONDITIONS

AU JOVINE R V M (Reprint); TRIPLETT E L; NELSON N B; PREZELIN B B

CS UNIV CALIF SANTA BARBARA, DEPT BIOL SCI, SANTA BARBARA, CA, 93106  
(Reprint); UNIV CALIF SANTA BARBARA, INST MARINE SCI, SANTA BARBARA, CA,

93106  
CYA USA  
SO PLANT AND CELL PHYSIOLOGY, (SEP 1992) Vol. 33, No. 6, pp. 733-741.  
ISSN: 0032-0781.  
DT Article; Journal  
FS LIFE; AGRI  
LA ENGLISH  
REC Reference Count: 29  
\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Absorption properties, pigmentation, total protein, apoprotein content, and isoelectric diversity of Peridinin-Chlorophyll a-Protein complexes (PCPs) and their apoproteins were determined for *Heterocapsa pygmaea* populations photoadapted to different spectral irradiances. Chromatic adaptation of pigmentation was evident and correlated more with quanta absorbed by the cells (AQ cell-1) than with quanta available in the surrounding light field (Qpar). Peridinin and chlorophyll content increased as blue-green and red light dosages declined respectively. Immunological determinations indicated PCP apoprotein abundance increased as AQ cell-1 decreased, while non-PCP protein content was unchanged. PCP apoproteins could account for up to 30% of total protein and exceed by 10-fold the amount required to bind all peridinin molecules into PCP complexes. Isoelectric variants of PCPs were identified, whose relative abundances were light dependent. Results are discussed in the context of future photoregulation studies of PCP gene expression in dinoflagellates.

L8 ANSWER 10 OF 11 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN  
AN 91:95081 SCISEARCH  
GA The Genuine Article (R) Number: EX038  
TI TETRAMERIC NATIVE STRUCTURE OF THE \*\*\*PERIDININ\*\*\* - \*\*\*CHLOROPHYLL\*\*\*  
\*\*\*A\*\*\* - \*\*\*BINDING\*\*\* \*\*\*PROTEIN\*\*\* FROM SYMBIODINIUM SP  
AU GERBERDING H (Reprint); NORRIS B; MILLER D J; MAYER F  
CS UNIV GOTTINGEN, INST MIKROBIOL, GRISEBACHSTR 8, W-3400 GOTTINGEN, GERMANY  
(Reprint); JAMES COOK UNIV N QUEENSLAND, DEPT CHEM & BIOCHEM, TOWNSVILLE,  
QLD 4811, AUSTRALIA  
CYA GERMANY; AUSTRALIA  
SO JOURNAL OF PLANT PHYSIOLOGY, (1991) Vol. 137, No. 3, pp. 285-290.  
DT Article; Journal  
FS LIFE; AGRI  
LA ENGLISH  
REC Reference Count: 20  
\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Electron microscopy of a single isoform of the \*\*\*peridinin\*\*\* -  
\*\*\*chlorophyll\*\*\* \*\*\*a\*\*\* - \*\*\*binding\*\*\* \*\*\*protein\*\*\* from  
Symbiodinium sp. indicates that the native structure is a tetrahedron-like  
assembly of four subunits. The subunits are elongated and have a somewhat  
bent appearance. Based on the EM observations, a working model is  
proposed that has two orthogonally-arranged dimers in contact via their  
concave surfaces.

L8 ANSWER 11 OF 11 DISSABS COPYRIGHT (C) 2004 ProQuest Information and  
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AN 2004:43470 DISSABS Order Number: AAI3110677  
TI Characterization and evolution of \*\*\*peridinin\*\*\* - \*\*\*chlorophyll\*\*\*  
\*\*\*a\*\*\* \*\*\*binding\*\*\* \*\*\*protein\*\*\* gene families in symbiotic  
dinoflagellates  
AU Reichman, Jay Randall [Ph.D.]; Hillis, David M. [advisor]; Vize, Peter D.  
[advisor]



CS The University of Texas at Austin (0227)  
 SO Dissertation Abstracts International, (2002) Vol. 64, No. 11B, p. 5366.  
 Order No.: AAI3110677. 176 pages.  
 DT Dissertation  
 FS DAI  
 LA English  
 ED Entered STN: 20040730  
 Last Updated on STN: 20040730

AB This dissertation consists of three integrated chapters. Chapter One presents the first genomic characterization of the PCP gene family from a symbiotic dinoflagellate, *Symbiodinium* sp. from *Hippopus hippopus* (*Symbiodinium* 203). *Symbiodinium* 203 has long PCP genes organized like those of *Amphidinium carterae* and *Lingulodinium polyedra*, but with a putative promoter that is different from *L. polyedra*. There are at least 14 distinct coding regions out of 36  $\pm$  12 PCP genes in this family. Diversity of *Symbiodinium* 203's PCP gene family appears to be consequence of low levels of concerted evolution and acts as a primary source of variability in PCP isoforms. Predicted amino acid substitutions in *Symbiodinium* 203's PCP apoproteins result in shifts of isoelectric points, and protein modeling suggests that polymorphic sites may influence light harvesting of holoproteins. In Chapter Two, the first PCP coding sequences from *S. pilosum*, *Symbiodinium* sp. from *Dichocoenia stokesii*, *S. pulchrorum* and *S. kawagutii* were presented. Diverse PCP gene families occur in all major clades of *Symbiodinium* and in both size classes of the gene. As with *Symbiodinium* 203 in Chapter One, these PCP gene families do not appear to have been homogenized through mechanisms leading to concerted evolution. The predicted PCP apoproteins from *S. pilosum* and *S. kawagutii* have calculated isoelectric focusing points that generally match values previously measured for these species, which supports the hypothesis that genetic polymorphism is the primary source generating differences in PCP isoforms. Protein modeling produced a putative tertiary structure for *S. pilosum* apoproteins and was used to identify polymorphic sites in *S. pilosum* and *S. kawagutii* PCPs that could affect spectral tuning of peridinin. And Chapter Three contains the first phylogenetic analyses of the evolution of dinoflagellate PCP gene families. The objective of this section is to estimate the selective pressure at the codon level within PCP genes. PCP polymorphism is ancient, however, the polymorphism is not maintained by positive selection. Codon sites within PCP genes are evolving under purifying selection and are subjected to net reduced levels of concerted evolution. Isoform diversity is probably selected for within a functional range.

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